

Sequence	Sequence	Description	Ratio	Fold Change	P-value	Sequence
YHR204W	MNL1,HTM	mannosidase like	4.96	4.96	0	SGD
YGL029W	CGR1	coiled-coil growth-regulated; coiled-coil protein; Null mutant is inviable, CGR1 expression is	3.9	3.9	1.47E-40	SGD
YBR018C	GAL7	galactose-1-phosphate uridylyl transferase; Null mutant is viable and cannot utilize galactose	3.16	3.16	2.29E-13	SGD
YKR097W	PCK1,JPM	phosphoenolpyruvate carboxylkinase; Null mutant is viable.	3.13	3.13	1.20E-09	SGD
YDR449C	YDR449C		2.81	2.81	7.43E-08	SGD
YHR205W	SCH9,KOM	protein kinase involved in growth control, may be redundant with cAMP pathway; cAMP-dep	2.45	2.45	3.13E-25	SGD
YDR213W	UPC2,MO	involved in sterol uptake; zinc finger transcription factor of the Zn(2)-Cys(6) binuclear cluste	2.39	2.39	3.10E-11	SGD
YBL109W	YBL109W		2.33	2.33	1.48E-12	SGD
YKL093W	MBR1	Involved in mitochondrial biogenesis; Null mutant is viable, shows defective growth on glyce	2.29	2.29	2.63E-16	SGD
YKR105C	YKR105C		2.16	2.16	1.36E-04	SGD
YAL025C	MAK16	putative nuclear protein; nuclear protein (putative); Null mutant is inviable, conditional mutar	2.11	2.11	3.35E-05	SGD
YFL027C	GYP8	GAP for Ypt protein; GTPase-activating protein; Null: viable	0.48	-2.1	7.92E-18	SGD
YKR027W	YKR027W		0.48	-2.1	7.84E-13	SGD
YEL071W	DLD3	D-lactate dehydrogenase	0.44	-2.29	9.75E-09	SGD
YOR273C	TPO4	Polyamine transport protein	0.43	-2.34	3.97E-34	SGD
YGL007W	YGL007W		0.36	-2.78	5.86E-09	SGD
YER103W	SSA4	member of 70 kDa heat shock protein family; HSP70 family; Null mutant is viable, ssa1 ssa:	2.1	2.1	3.63E-05	SGD
Q0070	AI5_ALPH	Intron of mitochondrial COX1, al5-alpha; DNA endonuclease involved in intron homing	2.24	2.24	7.42E-04	SGD
YMR169C	ALD3	Expression induced in response to heat shock, oxidative and osmotic stress. NAD+ is prefe	2.08	2.08	9.88E-13	SGD
YPL054W	LEE1	Product of gene unknown	2.08	2.08	7.78E-05	SGD
YNL036W	NCE103	involved in secretion of proteins that lack classical secretory signal sequences; An uncharac	2.42	2.42	0	SGD
YAL014C	YAL014C		2.24	2.24	0	SGD
YOR323C	PRO2	gamma-glutamyl phosphate reductase; Proline requiring and unable to grow on YPD (yeast	0.44	-2.28	8.53E-42	SGD
YKL060C	FBA1	aldolase; Null mutant is viable, lacks aldolase enzymatic activity and fails to grow in media c	0.41	-2.44	6.69E-24	SGD
YDR154C	YDR154C		0.38	-2.65	5.89E-04	SGD

Sequence	Accession	Primary Sequence Name	Description
634748	MNL1		BioProcess=biological_process unknown MolFunction=not yet annotated CellComponent=not yet annotated
635658	CGR1		BioProcess=biological_process unknown MolFunction=molecular_function unknown CellComponent=not yet annotated
633963	GAL7		BioProcess=not yet annotated MolFunction=molecular_function unknown CellComponent=not yet annotated
636201	PCK1		BioProcess=processing of 20S pre-rRNA MolFunction=snoRNA binding CellComponent=small nucleolar ribonucleoprotein complex
639393	YDR449C		BioProcess=biological_process unknown MolFunction=molecular_function unknown CellComponent=not yet annotated
638108	SCH9		BioProcess=galactose metabolism MolFunction=UTP-hexose-1-phosphate uridylyltransferase CellComponent=cytoplasm
638813	UPC2		BioProcess=biological_process unknown MolFunction=molecular_function unknown CellComponent=not yet annotated
633297	YBL109W		BioProcess=rRNA processing* MolFunction=molecular_function unknown CellComponent=nucleolus
633802	MBR1		BioProcess=ER-associated protein catabolism MolFunction=carbohydrate binding CellComponent=endoplasmic reticulum
637993	YKR105C		BioProcess=regulation of cell size MolFunction=protein serine/threonine kinase CellComponent=not yet annotated
638401	MAK16		BioProcess=steroid metabolism MolFunction=RNA polymerase II transcription factor CellComponent=cytoplasm
636872	GYP8		BioProcess=gluconeogenesis MolFunction=phosphoenolpyruvate carboxykinase (ATP) CellComponent=cytosol
636263	YKR027W		BioProcess=not yet annotated MolFunction=molecular_function unknown CellComponent=not yet annotated
637094	DLD3		BioProcess=biological_process unknown MolFunction=molecular_function unknown CellComponent=not yet annotated
638799	TPO4		BioProcess=polyamine transport MolFunction=spermine transporter CellComponent=vacuolar membrane
637490	YGL007W		BioProcess=lactate metabolism MolFunction=D-lactate dehydrogenase (cytochrome) CellComponent=cytoplasm*
635424	SSA4		BioProcess=stress response* MolFunction=chaperone* CellComponent=cytoplasm
970792	AI5_ALPH		BioProcess=biological_process unknown MolFunction=molecular_function unknown CellComponent=not yet annotated
633415	ALD3		BioProcess=stress response MolFunction=aldehyde dehydrogenase CellComponent=cytoplasm
635078	LEE1		BioProcess=biological_process unknown MolFunction=molecular_function unknown CellComponent=not yet annotated
634452	NCE103		BioProcess=not yet annotated MolFunction=molecular_function unknown CellComponent=cytoplasm
639165	YAL014C		BioProcess=biological_process unknown MolFunction=molecular_function unknown CellComponent=not yet annotated
636109	PRO2		BioProcess=proline biosynthesis MolFunction=glutamate-5-semialdehyde dehydrogenase CellComponent=cytoplasm
639349	FBA1		BioProcess=gluconeogenesis* MolFunction=fructose-bisphosphate aldolase CellComponent=cytoplasm*
639037	YDR154C		BioProcess=biological_process unknown MolFunction=molecular_function unknown CellComponent=not yet annotated